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AUG 23 2001

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: DLO-Center for Plant Breeding and
Reproduction Research
- (B) STREET: Droevedaalsesteeg 1
- (C) CITY: Wageningen
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 6708 PB
- (G) TELEPHONE: +31 317 477001
- (H) TELEFAX: +31 317 418094
- (I) TELEX: -

(ii) TITLE OF INVENTION: A method for plant protection against insects
or nematodes

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/NL98/00352

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Actinia equina

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 99..695

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..695

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:3..98

(ix) FEATURE:
(A) NAME/KEY: 5'UTR
(B) LOCATION:1..2

(ix) FEATURE:
(A) NAME/KEY: 3'UTR
(B) LOCATION:696..888

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Gruden, Kristina
Strukelj, Borut
Popovic, Tatjana
Lenarcic, Brigita
Bevec, Tadeja
Brzin, Joze
Kregar, Igor
Herzog-Velikonja, Jana
Stiekema, Willem J
Bosch, Dirk
(B) TITLE: The cysteine protease activity of Colorado
potato beetle (*Leptinotarsa decemlineata*) guts,
which is insensitive to potato protease
inhibitors, is inhibited by thyroglobulin type-1
domain inhibitors
(C) JOURNAL: Insect Biochem. Mol. Biol
(D) VOLUME: 28
(F) PAGES: 549-560
(G) DATE: 1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CT ATG GCT CTT AGC CAA AAC CAA GCC AAG TTT TCC AAA GGA TTC GTC	47
Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val	
-32 -30 -25 -20	
GTG ATG ATT TGG GTA CTA TTC ATT GCT TGT GCT ATA ACT TCA ACT GAA	95
Val Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu	
-15 -10 -5	
GCT AGT CTA ACC AAA TGC CAA CAG CTC CAG GCC TCG GCT AAC AGT GGT	143
Ala Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly	
1 5 10 15	
CTG ATA GGT ACT TAT GTA CCA CAA TGC AAA GAA ACG GGA GAG TTC GAA	191
Leu Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu	
20 25 30	
GAA AAA CAA TGC TGG GGA TCG ACT GGT TAC TGT TGG TGT GTG GAT GAA	239
Glu Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu	
35 40 45	

GAT GGA AAA GAG ATT CTA GGA ACC AAG ATC CGT GGA TCT CCG GAT TGC Asp Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys	287
50 55 60	
AGC CGC AGA AAA GCC GCG TTA ACA CTT TGC CAG ATG ATG CAA GCC ATC Ser Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile	335
65 70 75	
ATT GTT AAT GTC CCT GGT TGG TGT GGC CCT CCA TCG TGT AAA GCT GAC Ile Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp	383
80 85 90 95	
GGC AGT TTT GAC GAG GTT CAG TGC TGC GCA AGT AAT GGA GAA TGC TAC Gly Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr	431
100 105 110	
TGT GTG GAT AAG AAA GGA AAA GAA CTT GAA GGC ACA AGA CAA CAG GGA Cys Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly	479
115 120 125	
AGG CCA ACC TGC GAA AGA CAC CTA AGC GAA TGC GAG GAA GCT CGA ATC Arg Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Ala Arg Ile	527
130 135 140	
AAG GCG CAT TCA AAC AGT CTT CGT GTT GAG ATG TTC GTG CCA GAG TGT Lys Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys	575
145 150 155	
TTA GAA GAT GGA TCA TAT AAC CCA GTA CAG TGC TGG CCT AGC ACA GGA Leu Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly	623
160 165 170 175	
TAC TGT TGG TGC GTC GAT GAA GGA GGG GTA AAG GTA CCA GGT TCC GAT Tyr Cys Trp Cys Val Asp Glu Gly Val Lys Val Pro Gly Ser Asp	671
180 185 190	
GTC AGA TTT AAA CGC CCC ACA TGC TAAGAAAAAC ACAGTGAACA AAGTGGCTAG Val Arg Phe Lys Arg Pro Thr Cys	725
195	
TTTCCAGATC GAAAATAACT ACAAAAGGATT AATAAAATGT TAAAATAATT TCTCAATTG	785
GCTGTGATAT ATTTTTCCA AGATAATTG ATCTGCATGT AGTTAACAGA AAACAATCTC	845
AACTAGAAAT AAAGACTACG GTAATAATGA CAAAAAAA AAA	888

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val Val
 -32 -30 -25 -20

Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Thr Glu Ala
-15 -10 -5

Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu
 1 5 10 15

Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu
 20 25 30

Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu Asp
 35 40 45

Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser
50 55 60

Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile
65 70 75 80

Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly
85 90 95

Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys
 100 105 110

Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg
115 120 125

Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile Lys
130 135 140

Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu
145 150 155 160

Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr
165 170 175

Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val
 180 185 190

Arg Phe Lys Arg Pro Thr Cys
185

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Actinia equina*

(vii) IMMEDIATE SOURCE:
(B) CLONE: optimized gene for expression in plants

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..693

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:97..693

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:1..693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCT CTT AGC CAG AAC CAG GCC AAG TTT TCC AAG GGA TTC GTC GTG	48
Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val Val	
-32 -30 -25 -20	

ATG ATT TGG GTA CTA TTC ATT GCT TGT GCT ATC ACT TCA ACT GAA GCT	96
Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu Ala	
-15 -10 -5	

AGT CTA ACG AAA TGC CAA CAG CTG CAG GCC TCG GCT AAC AGT GGT CTG	144
Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu	
1 5 10 15	

ATA GGT ACT TAT GTA CCA CAA TGC AAA GAA ACT GGA GAG TTT GAA GAA	192
Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu	
20 25 30	

AAG CAA TGC TGG GGA TCG ACT GGT TAC TGT TGG TGT GTG GAT GAA GAT	240
Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu Asp	
35 40 45	

GGA AAA GAG ATT CTA GGT ACA AAG ATC CGT GGA TCT CCA GAC TGC AGT Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser	288
50 55 60	
CGC AGA AAA GCT GCC TTA ACA CTT TGC CAG ATG ATG CAA GCC ATC ATT Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile	336
65 70 75 80	
GTG AAT GTC CCT GGT TGG TGT GGA CCT CCA TCA TGT AAA GCT GAC GGC Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly	384
85 90 95	
AGT TTT GAC GAG GTT CAG TGC TGC GCA AGT AAT GGA GAA TGC TAC TGT Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys	432
100 105 110	
GTG GAT AAG AAA GGA AAA GAA CTT GAA GGC ACA AGA CAA CAG GGA AGG Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg	480
115 120 125	
CCA ACC TGC GAA AGA CAC CTA AGC GAA TGC GAG GAG GCT CGT ATC AAG Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Ala Arg Ile Lys	528
130 135 140	
GCA CAT TCA AAC AGT CTT CGT GTT GAG ATG TTC GTG CCA GAG TGT TTA Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu	576
145 150 155 160	
GAA GAT GGA TCT TAC AAC CCT GTA CAG TGC TGG CCT AGC ACA GGA TAC Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr	624
165 170 175	
TGT TGG TGC GTC GAT GAA GGA GGG GTA AAG GTT CCA GGT TCC GAC GTC Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val	672
180 185 190	
AGA TTC AAA CGT CCC ACA TGC TAA Arg Phe Lys Arg Pro Thr Cys	696
195	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Ala	Leu	Ser	Gln	Asn	Gln	Ala	Lys	Phe	Ser	Lys	Gly	Phe	Val	Val
-32		-30					-25						-20		

Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu Ala
 -15 -10 -5

Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu
1 5 10 15

Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu
20 25 30

Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val 'Asp Glu Asp
 35 40 45

Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser
 50 55 60

Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile

Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly

Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys

Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg

Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile Lys

Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu

Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr

Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val

Arg Phe Lys Arg Pro Thr Cys